

Year	Age	Sex	Location	Case No.	Ref.
1971	10-14	M	India	1	[1]
1972	10-14	M	India	2	[2]
1973	10-14	M	India	3	[3]
1974	10-14	M	India	4	[4]
1975	10-14	M	India	5	[5]
1976	10-14	M	India	6	[6]
1977	10-14	M	India	7	[7]
1978	10-14	M	India	8	[8]
1979	10-14	M	India	9	[9]
1980	10-14	M	India	10	[10]
1981	10-14	M	India	11	[11]
1982	10-14	M	India	12	[12]
1983	10-14	M	India	13	[13]
1984	10-14	M	India	14	[14]
1985	10-14	M	India	15	[15]
1986	10-14	M	India	16	[16]
1987	10-14	M	India	17	[17]
1988	10-14	M	India	18	[18]
1989	10-14	M	India	19	[19]
1990	10-14	M	India	20	[20]
1991	10-14	M	India	21	[21]
1992	10-14	M	India	22	[22]
1993	10-14	M	India	23	[23]
1994	10-14	M	India	24	[24]
1995	10-14	M	India	25	[25]
1996	10-14	M	India	26	[26]
1997	10-14	M	India	27	[27]
1998	10-14	M	India	28	[28]
1999	10-14	M	India	29	[29]
2000	10-14	M	India	30	[30]
2001	10-14	M	India	31	[31]
2002	10-14	M	India	32	[32]
2003	10-14	M	India	33	[33]
2004	10-14	M	India	34	[34]
2005	10-14	M	India	35	[35]
2006	10-14	M	India	36	[36]
2007	10-14	M	India	37	[37]
2008	10-14	M	India	38	[38]
2009	10-14	M	India	39	[39]
2010	10-14	M	India	40	[40]
2011	10-14	M	India	41	[41]
2012	10-14	M	India	42	[42]
2013	10-14	M	India	43	[43]
2014	10-14	M	India	44	[44]
2015	10-14	M	India	45	[45]
2016	10-14	M	India	46	[46]
2017	10-14	M	India	47	[47]
2018	10-14	M	India	48	[48]
2019	10-14	M	India	49	[49]
2020	10-14	M	India	50	[50]

CLASS A GROUP II						
A1AB_human	α_{1B} -adrenergic alpha 1B-AR		TMDI junction between TMDIII and IC2	63 FAIVGNILVIL A 142 CAISIDRYIGV A 143 CAISIDRYIGV K	IP / COS-7	(Scheer, Fanelli et al. 1997)
A1AB_human	α_{1B} -adrenergic		junction between TMDIII and IC2		IP / COS-7	(Scheer, Costa et al. 2000)
A1AB_human	alpha 1B-AR α_{1B} -adrenergic		TMIII carboxyl end of IC3 TMV	128 AVDVLCCCTASI F 293 REKKA A KTGLI E 204 E E PFYALFSSLG V	IP / COS-1 IP arachidonic acid release IP / COS-1	(Perez, Hwa et al. 1996) (Hwa, Gaivin et al. 1997)
A1AB_human	α_{1B} -adrenergic		C-terminal IC3	293 SREKKA A KT X=19 different substitutions	PI / COS-7	(Kjelsberg, Cotecchia et al. 1992)
A1AB_human	α_{1B} -adrenergic		C-terminus IC3	288 293 KFSREKKA A KTGLI K H L	PI hydrolysis / rat fibroblast	(Allen, Lefkowitz et al. 1991)
A2AA_human	α_2 C10-adrenergic		C-terminal IC3 loop	373 (348?) EKRF T FVLAV X=F, A, C, E, K	adenylyl cyclase inhibition / HEK293	(Ren, Kurose et al. 1993)
ACM1_human	alpha-2AAR muscarinic Hm1		C-terminal IC3 loop junction	360 SLVKEKKA E AARTLS A	PI / HEK(U293)	(Högger, Shockley et al. 1995)
ACM2-human	muscarinic acetylcholine M1 muscarinic acetylcholine M2		junction of IC3 and TMVI	390 KKVTRTIL T A 1-4 A inserted	IP production, inhibition of cAMP production / COS-7	(Liu, Blin et al. 1996)

Figure 1 (Page 2 of 15)

CLASS A GROUP II							
ACM3_rat	m3 muscarinic (rat)	TMVI		507 TWTPYNIMVLVNT S	IP / COS-7		(Blüml, Mutschler et al. 1994)
ACM5_human	muscarinic acetylcholine M3 m5 muscarinic	N-terminus to TMII TMVI		chimera composed of m2 1-69 m5 77-445 m2 391-466	β-gal / NIH 3T3		(Burststein, Spalding et al. 1996)
ACM5_human	muscarinic acetylcholine M5 m5 muscarinic	TMVI		451 459 465 AIIIA FIITW TPYNIMVLVST M L H C V S F T	β-gal; radioligand binding / NIH-3T3		(Spalding, Burststein et al. 1998)
ACM5_human	muscarinic acetylcholine M5	junction of TMVI and EC3		465 YNIMVLVSTFCDKCV X=V,F,R,K,+more	β-gal; radioligand binding / NIH-3T3		(Spalding, Burststein et al. 1997)
B1AR_human	m5 muscarinic muscarinic acetylcholine M5	C-terminus		389 RKAFQGLLCCA R	adenylyl cyclase; agonist binding / CHW		(Mason, Moore et al. 1999)
B2AR_human	β ₂ -adrenergic beta-2AR	C-terminal IC3 loop		266 272 FCLKEHKALKTGLI SR K A	adenylyl cyclase activation; agonist binding affinity / COS-7 or CHO		(Samama, Cotecchia et al. 1993); (Lefkowitz, Cotecchia et al. 1993)
DADR_human	dopamine D1A	carboxyl terminal IC3		264 SFKMSFKRETQVLKT I K 288 from D1B receptor APDTSIKKETKVLKT	adenylyl cyclase; cAMP accumulation / HEK293		(Charpentier, Jarvie et al. 1996)
DADR_human	dopamine D1	TMVI		286 FVCCWLPPFFIL A	CAMP accumulation / COS-7		(Cho, Taylor et al. 1996)
HH2R_rat	histamine H ₂	IC2		115 FMISLDRYCAV N, A	cAMP production / HEK-293		(Alewijns, Timmerman et al. 2000)

Figure 1 (Page 3 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP III OPSD_human	opsin rhodopsin	TMII TMIII TMVII	90 FMVLGGFTSTLY D 113 GCNLEGGFFAT Q 292 296 MTIPAFFAKSAIY E G, E, M 292 Ala neutral a.a converted to carboxylate and competes with ¹¹³ Glu for salt bridge with ²⁹⁶ Lys	transducin; phosphorylation by rhodopsin kinase / COS	(Rim and Oprian 1995)
OPSD_human	opsin rhodopsin	TMIII	134 VVLAIERYVVV I, Q, S	transducin; radioligand binding / COS	(Acharya and Karnik 1996)
OPSD_human	opsin rhodopsin	TM6	257 RMVIMVIAFL Y, N	transducin, GTP- γ S uptake / COS	(Han, Smith et al. 1998)
OPSD_human	opsin rhodopsin	plus TM3 TMVII	plus G113Q 296 PAFFAKSAIY G X=E, M natural mutants + 10 different a.a. substitutions disrupts critical salt bridge between ²⁹⁶ Lys(TMVII) and ¹¹³ Glu(TMIII)	transducin; radioligand binding / COS	(Govardhan and Oprian 1994); (Cohen, Yang et al. 1993)
		IC2	134 VVLAIERYVVV Q		(Cohen, Yang et al. 1993)

Figure 1 (Page 4 of 15)

TRFR_mouse	thyrotropin-releasing hormone TRH-R	carboxyl tail	335 FRKL C NCCKQK STOP	⁴⁵ Ca ²⁺ efflux, [Ca ²⁺] / Xenopus oocytes; IP formation / AIT20, <i>stably transfected</i>	(Matus-Leibovitch, Nussenzveig et al. 1995)

Figure 1 (Page 5 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP IV BRB2_human	bradykinin B ₂ B2 bradykinin BK-2	TMIII TMVI	113 ATISMNLYSSI A 256 LLFICNLPFQI F	IP production / COS-7	(Marie, Koch et al. 1999)

Figure 1 (Page 6 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A					
GROUP V					
AG2R_rat	AT _{1A} Type-1A angiotensin II	TMIII	111 ASVSFNL ^A YASV disrupts ¹¹¹ Asn (TMIII) - ²⁹² Tyr (TMVII) interaction	phospholipase C; IP production / COS-7	(Grobowski, Maigret et al. 1997)
AG2R_rat	AT _{1A}	C-terminus of TM7	305 LFYGF ^Q LGGKFK	IP production / HEK-293; intracellular Ca ²⁺ mobilization / CHO	(Parnot, Bardin et al. 2000)
FMLR_human	Type-1A angiotensin II formylmethionylleucylphenylalanine (fMLPR)	other multiple mutations IC1	51 LVIVWAGFRMTHTVT ^I ISYLNKAVA LVVWVTAF ^E AKRTINAIWFLNLAVA (K above conflicts with SWISS-PROT database)	PI production; phospholipase C stimulation / COS-7	(Amatruda, Dragas-Graonic et al. 1995)
IL8B_human	interleukin-8 receptor B	IC2	138 ACISVD ^R RYLAIVH V	IP production; Ca ²⁺ mobilization and actin polymerization / NIH 3T3	(Burger, Burger et al. 1999)
L5HR_human	CXCR-2 chemokine	IC3	564 MATNKDT ^G KIAKK	cAMP production / HEK293	(Kudo, Osuga et al. 1996)
L5HR_human	luteinizing hormone (LH)	TMVI	578 ILIFTD ^G FTCMA	cAMP production / COS-7	(Shenker, Laje et al. 1993)
L5HR_human	luteinizing hormone (LH)	TM6	571 577 KI ^I AKKMAILIFTD ^I FTCM	cAMP production / COS-7	(Kosugi, Van Dop et al. 1995)
L5HR_rat	luteinizing hormone / human chorionic gonadotropin (LH/hCG)	TMVI	556 ILIFTD ^{G, Y} FTCMA	cAMP production / HEK 293T	(Bradbury, Kawate et al. 1997; Bradbury and Menon 1999)
OPRD_mouse	delta opioid receptor	TM3	128 KVLSD ^{A, K, H} YNNMF	adenyl cyclase inhibition / COS-7	(Cavalli, Babey et al. 1999)
OXYR_human	oxytocin	IC2	137 LMSLD ^A RCLAI ^C	IP production / COS-7	(Fanelli, Barbier et al. 1999)

Figure 1 (Page 7 of 15)

PAFR_human	platelet-activating factor (PAF)	C-terminus of IC3	231 EVKRRALMMVCTVLAV R	IP production / COS-7	(Parent, Le Gouill et al. 1996)
PAFR_human	platelet-activating factor (PAF)	TMIII	100 CLFFINTYCSV A	arachidonate release, IP production, adenylyl cyclase inhibition / CHO inhibition of adenylyl cyclase / CHO-K1	(Ishii, Izumi et al. 1997)
PE23_human	prostaglandin E ₃ , EP3III, EP3IV	C-terminal tail	360 FCOEEFWGN FCOMRKRRRLREOEEFWGN ↑truncated		(Jin, Mao et al. 1997)
PE23_mouse	prostaglandin E ₃ , EP3	carboxyl-terminal tail	336 KILLRKFCQIRDHT (3α) MMNHL (3β) ↑truncated	inhibition of adenylyl cyclase / CHO, stably expressed	(Hasegawa, Negishi et al. 1996)
THRR_human	thrombin	EC2 loop	259 CHDVLNETLLEGYYVY DLKD KDF I	⁴⁵ Ca ²⁺ efflux, PI hydrolysis, reporter gene induction / COS-7	(Nanevicz, Wang et al. 1996)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	EC1 EC2	486 YYNHAIDWQTG F, M 568 YAKVSI ^T CLPMD	inositol phosphate--diacylglycerol cascade / COS-7	(Parma, Van Sande et al. 1995)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMIII TMVII	509 ASELSVYTLTV A 672 YPLNSCANPFL Y	adenylyl cyclase activation / COS-7	(Duprez, Parma et al. 1994)
TSHR_human	thyrotropin (TSHR)	TMV	597 VAFVIVCCCHV L	cAMP formation / COS-7 cells	(Esapa, Duprez et al. 1999)
TSHR_human	thyroid stimulating hormone thyrotropin (TSHR)	TMVII	677 CANPFLYAIFT V	cAMP formation / CHO cells	(Russo, Wong et al. 1999)
TSHR_human	thyroid stimulating hormone thyrotropin (TSHR)	IC3	613 VRNPQYNPGDKDTKIAK 621 deletion	cAMP formation / COS-7	(Wonerow, Schoneberg et al. 1998)

Figure 1 (Page 8 of 15)

TSHR_human	thyrotropin (TSHR)	IC3 / TMVI	623 632 KDTKIAKRMVAVLIITDFICM V I	cAMP activation / COS-7	(Paschke, Tonacchera et al. 1994)
V2R_human	thyroid stimulating hormone vasopressin V2	IC2	136 LAMTLDRHRAI A	cAMP formation / COS-7	(Morin, Cotte et al. 1998)

Figure 1 (Page 9 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS B GROUP I CALR_human	human calcitonin hCTR-1 hCTR-2	wild type (native) protein		adenylyl cyclase cAMP production / COS-1	(Cohen, Thaw et al. 1997)
CLASS B GROUP II PTRR_human	parathyroid hormone PTH / PTH-related peptide	junction of IC1 and TMII junction of IC3 and TMVI	223 TRNYIH ^u MHLFL R, K 410 KLLKSTLVLMP C, others	cAMP accumulation / COS-7	(Schipani, Jensen et al. 1997)
CLASS B GROUP III GIPR_human	glucose-dependent insulinotropic peptide (GIP-R)	TMVI	340 VFAPVTEE ^u QAR P	cAMP production / L293	(Tseng and Lin 1997)
GLR_rat	glucagon	junction of IC loop1 and TMII IC end of TMVI	178 TRNYIH ^u GNLFA R 352 RLARST ^u LLIP A	cAMP accumulation / COS-7	(Hjorth, Ørskov et al. 1998)
VIPR_human	vasoactive intestinal peptide 1 (VIP)	junction of IC loop 1 and TMII junction of IC loop 3 and TMVI	178 RNYIH ^u MHLFI R functional integrity of the N-terminal EC domain 343 LARST ^u LLIP X= K, P	cAMP production / COS-7 or CHO	(Gaudin, Maoret et al. 1998) (Gaudin, Rouyer-Fessard et al. 1998)

Figure 1 (Page 10 of 15)

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS D Q74283 RCB2 C. cinereus STE2_yeast	pheromone	TM6	229 PLSAYQIYLG P	heterologous yeast assay	(Olesnicky, Brown et al. 1999)
STE2_yeast	pheromone α -factor	TM6	258 QSLLVPSIIFI LL	<i>lacZ</i> reporter gene	(Konopka, Margarit et al. 1996)
STE2_yeast	pheromone α -factor	double mutations TM5 and TM6	223 MSFVLVVKILLAIR C C 247 251 DSFHILLIQCSSL CC CC double mutations TM5 and TM6	<i>lacZ</i> reporter gene / yeast	(Dube, DeCostanzo et al. 2000)
STE3_yeast	pheromone α -factor	IC3	194 DVRDILHCTNS Q	β -galactosidase	(Boone, Davis et al. 1993)
STE2_yeast	pheromone α -factor	TM6	253 258 LIMSCQSLLVPSIIFI L LP	β -galactosidase	(Sommers, Martin et al. 2000)

Figure 1 (Page 12 of 15)

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Figure 1 (Page 13 of 15)

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Figure 1 (Page 14 of 15)

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Figure 1 (Page 15 of 15)

A Point Mutation Enhances MC-4 Receptor Constitutive Activity

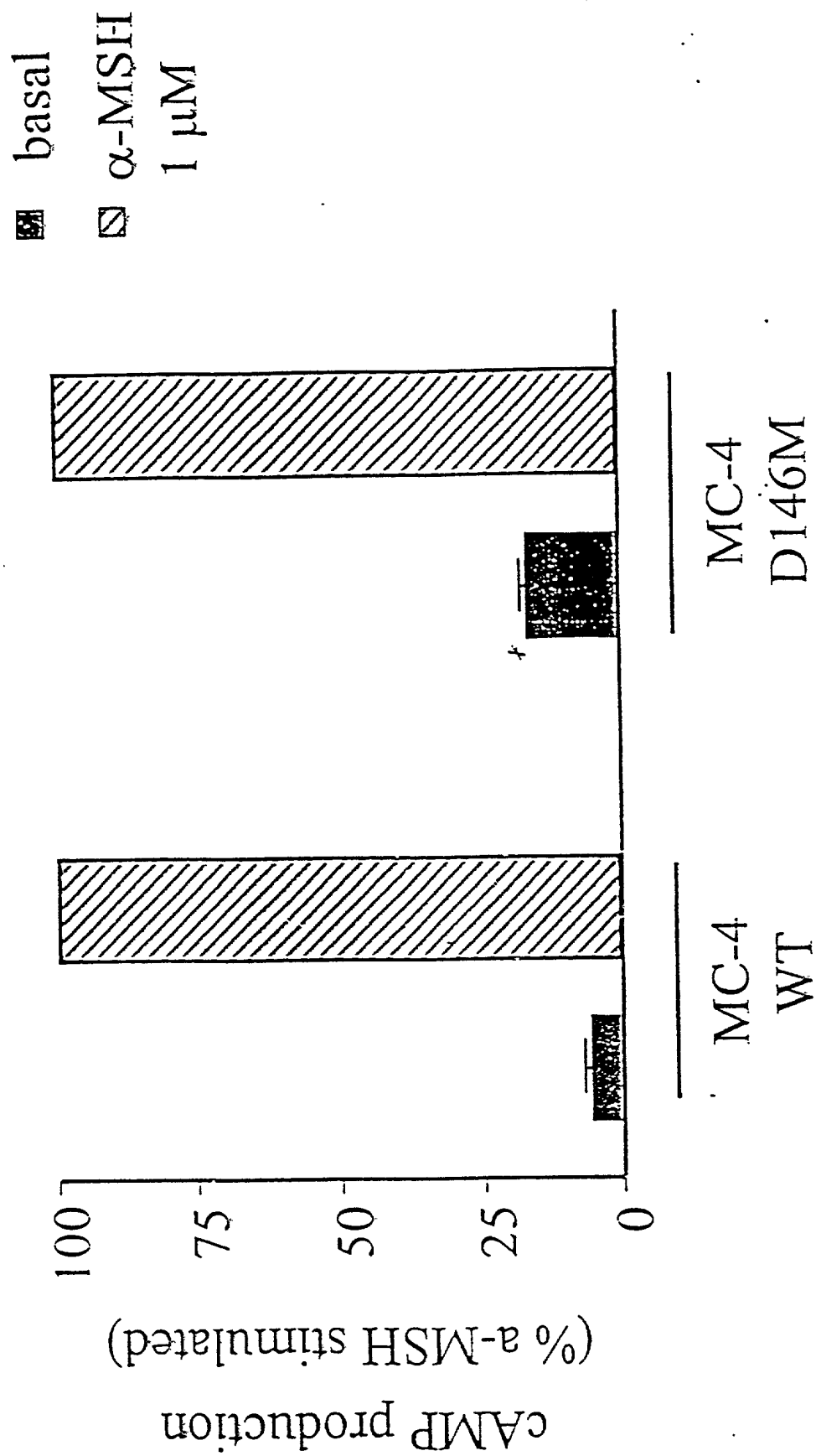


Figure 2

Light Emission Induced by the WT CCK-BR vs. a Constitutively Active Mutant

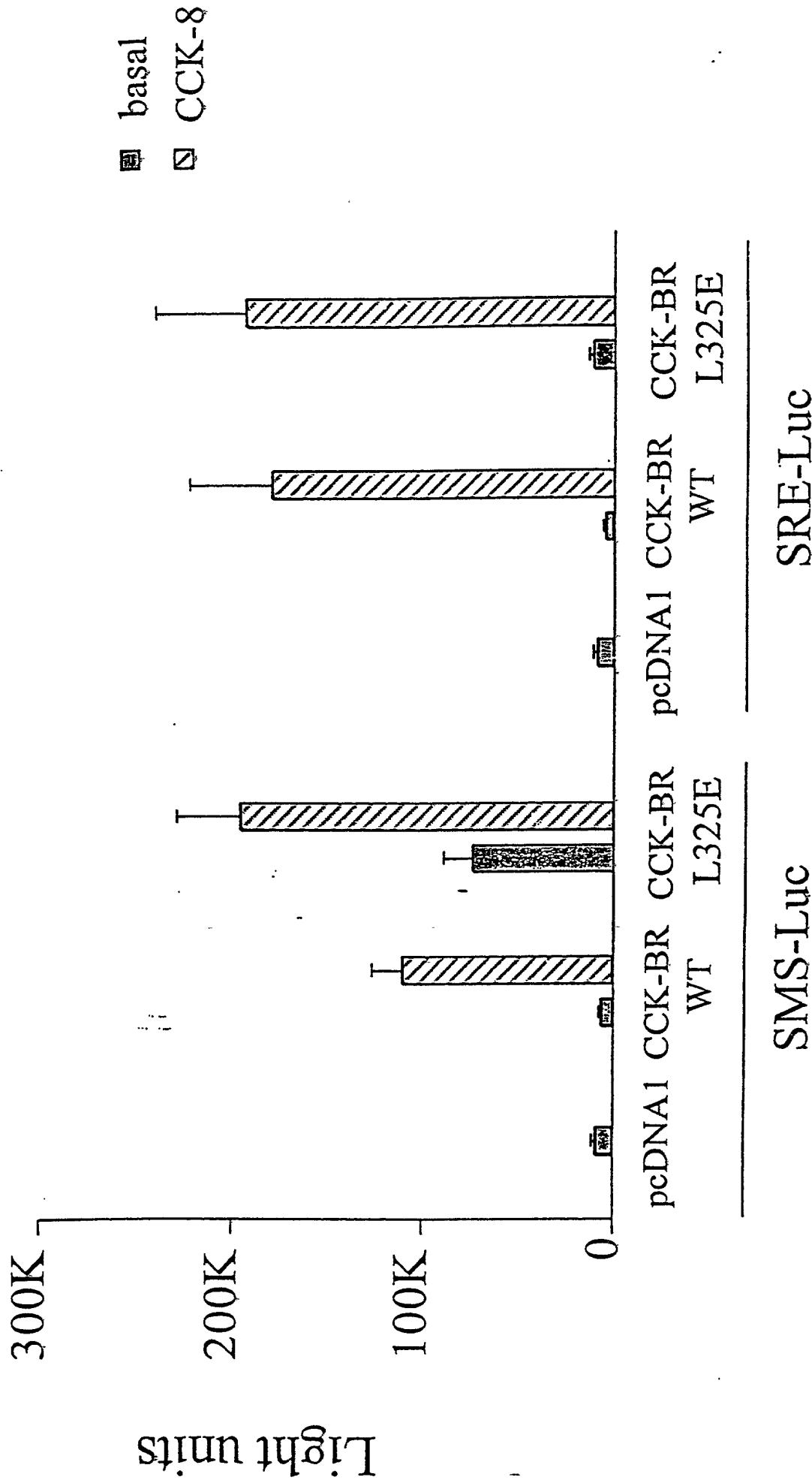


Figure 3

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor

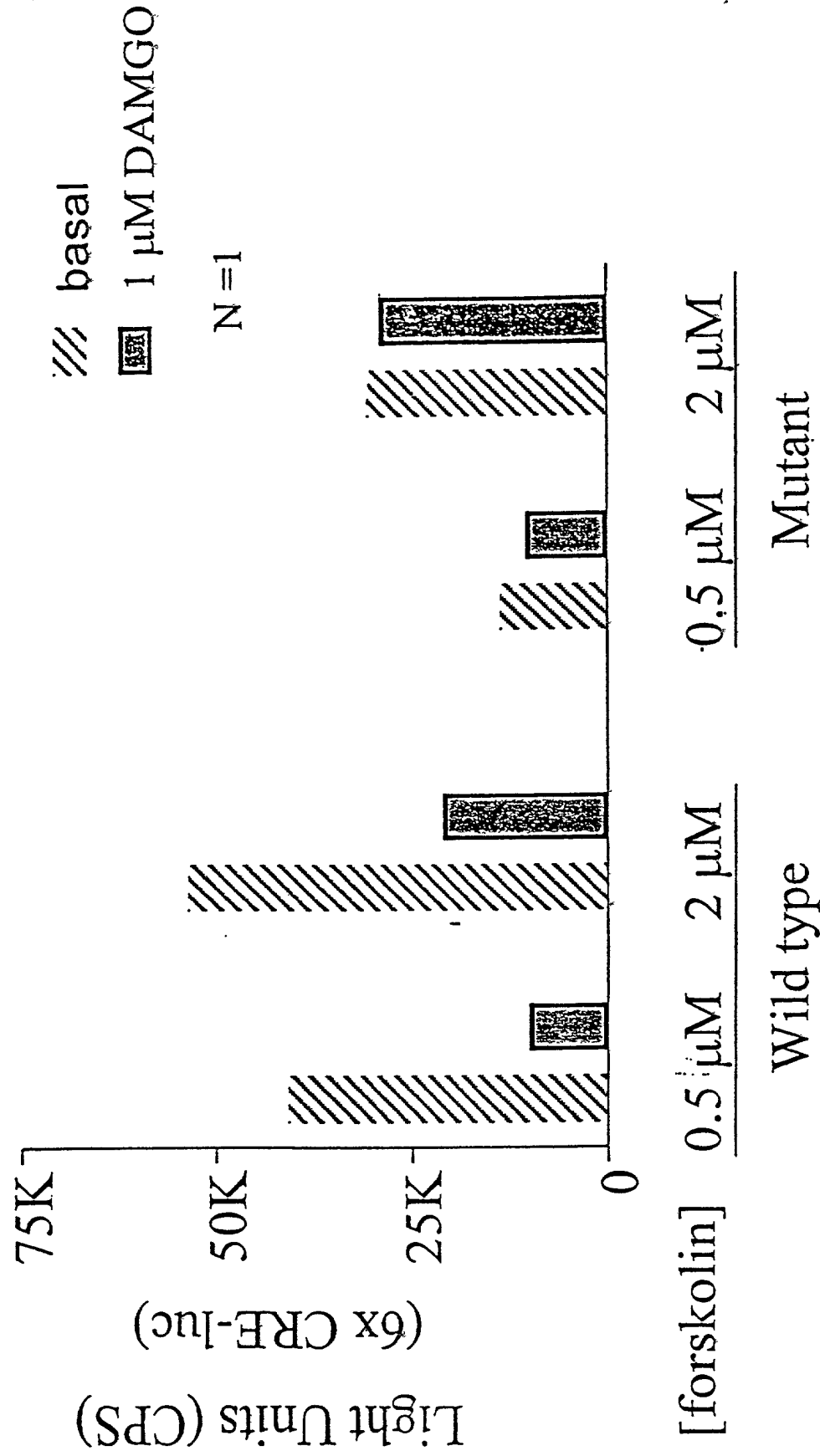


Figure 4

Forskolin Stimulated HEK293 Cells Transfected With pcDNA1 and a CRE-luc Construct

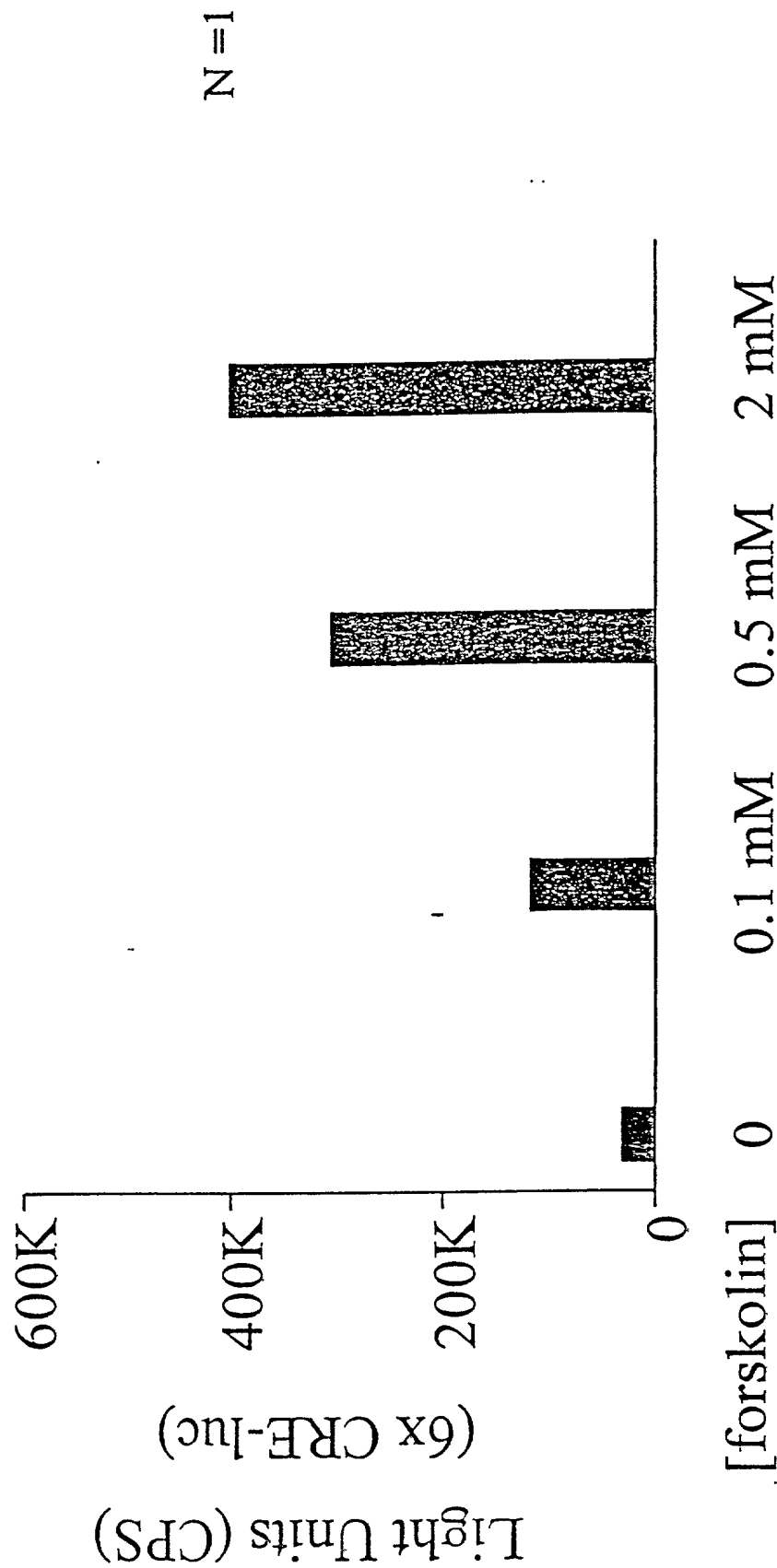


Figure 5

The Rat μ Opioid Receptor Signals Through G α i



Figure 6

A Point Mutation Confers Constitutive Activity to the Rat μ Opioid Receptor

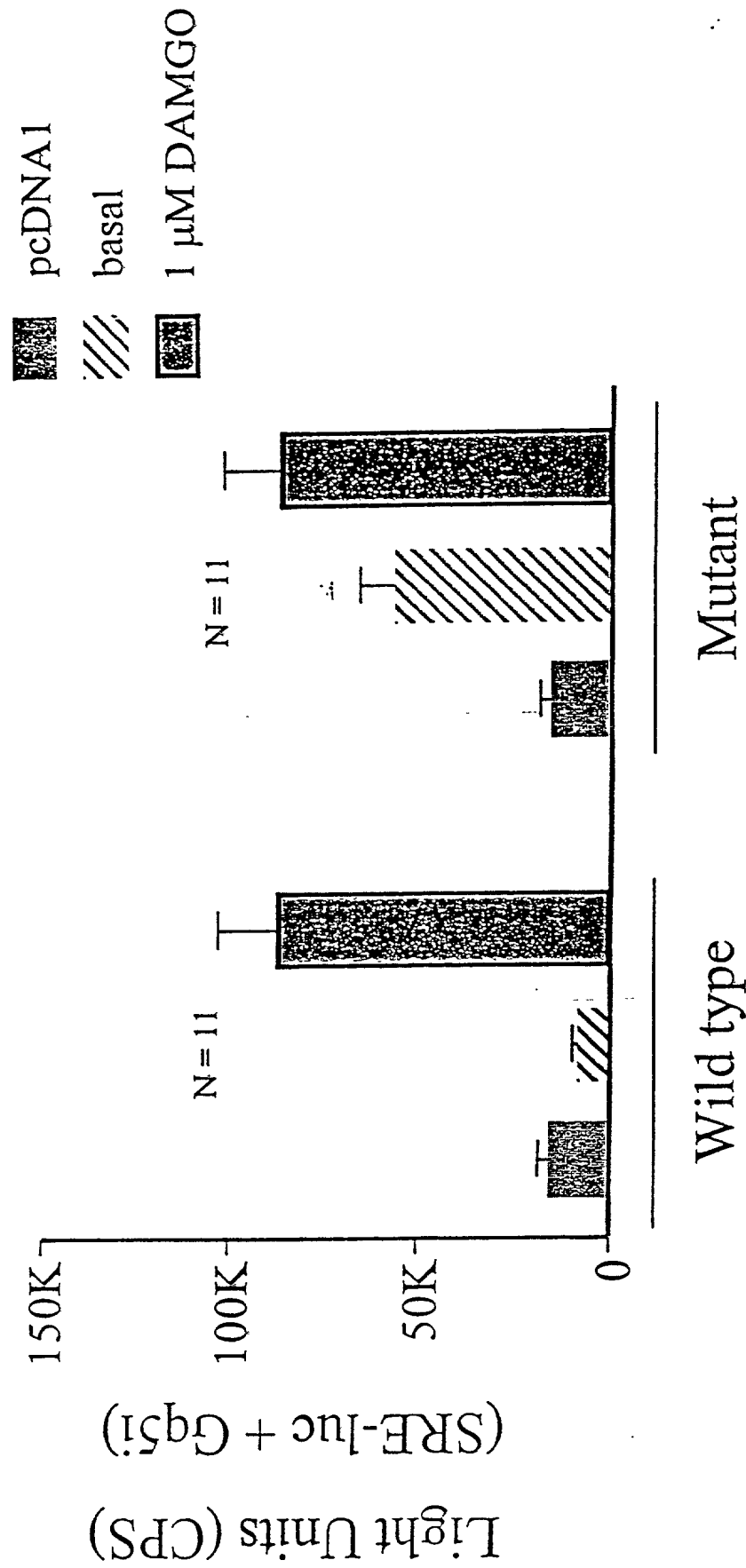


Figure 7

Target Residues Within Class I GPCRs

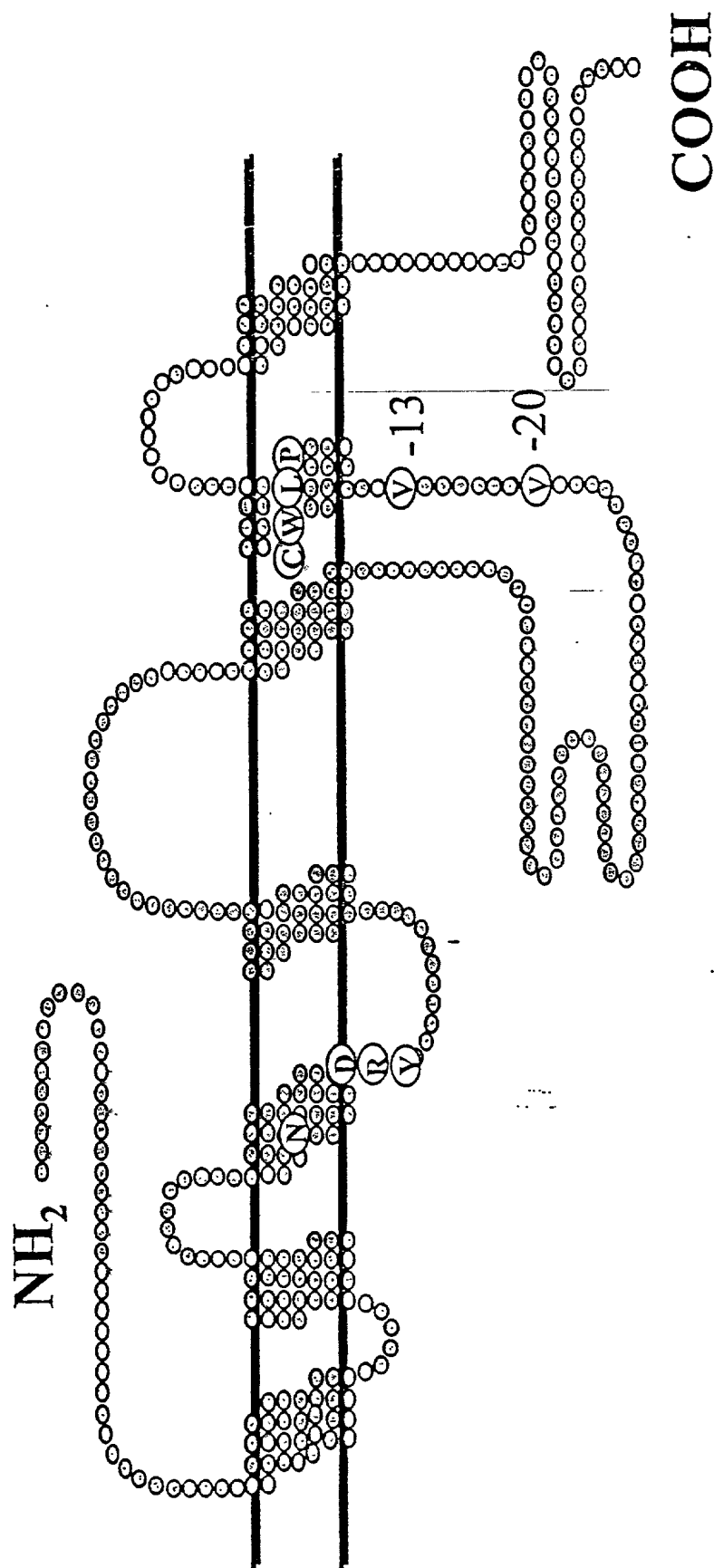


Figure 8

The 'DRY' Motif is a Target for Mutation

Induced Constitutive Activity

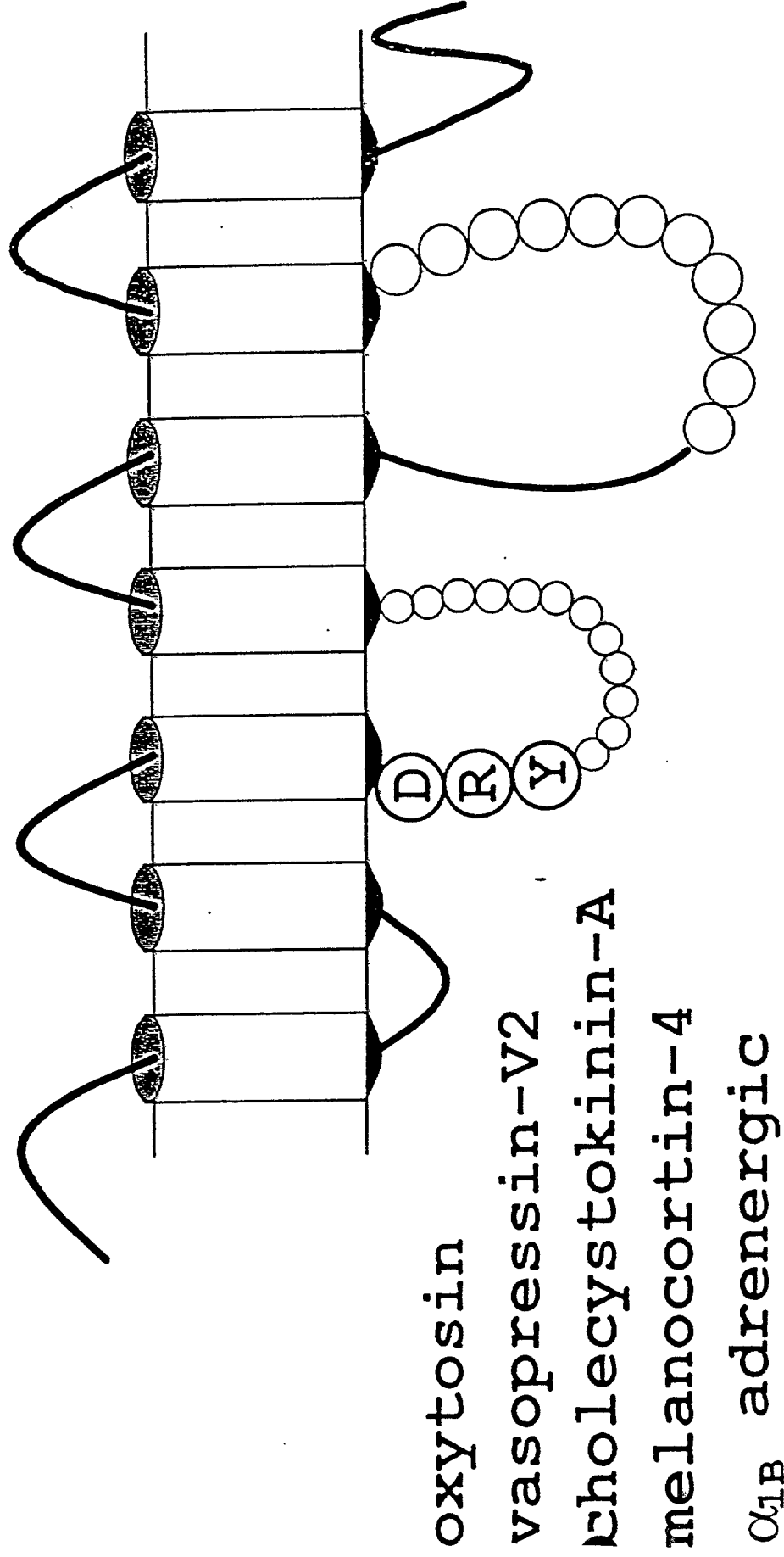


Figure 10

A Point Mutation Enhances MC-4 Receptor Constitutive Activity

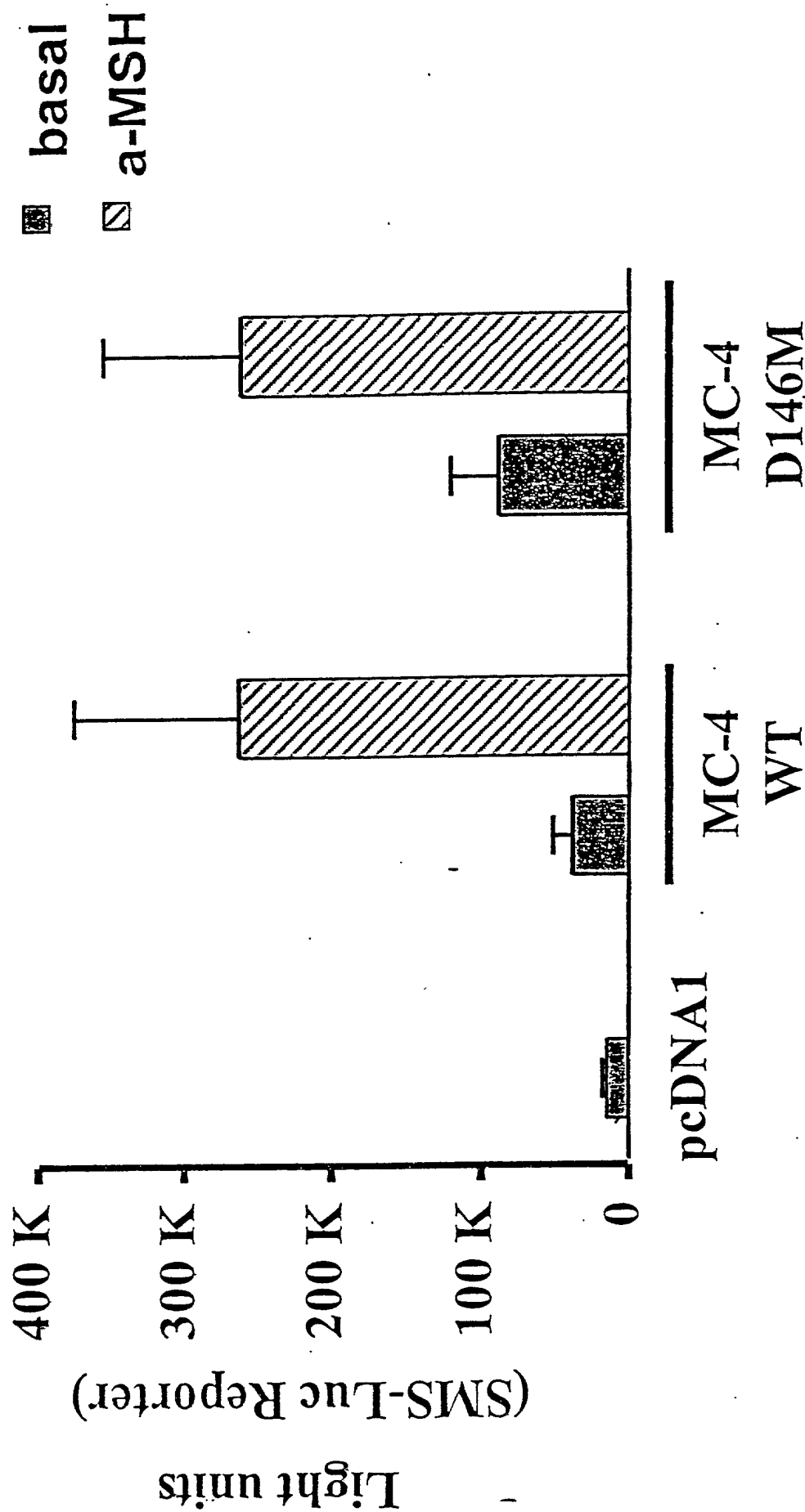


Figure 11

The -13 Position is a Target for Mutation Induced Constitutive Activity

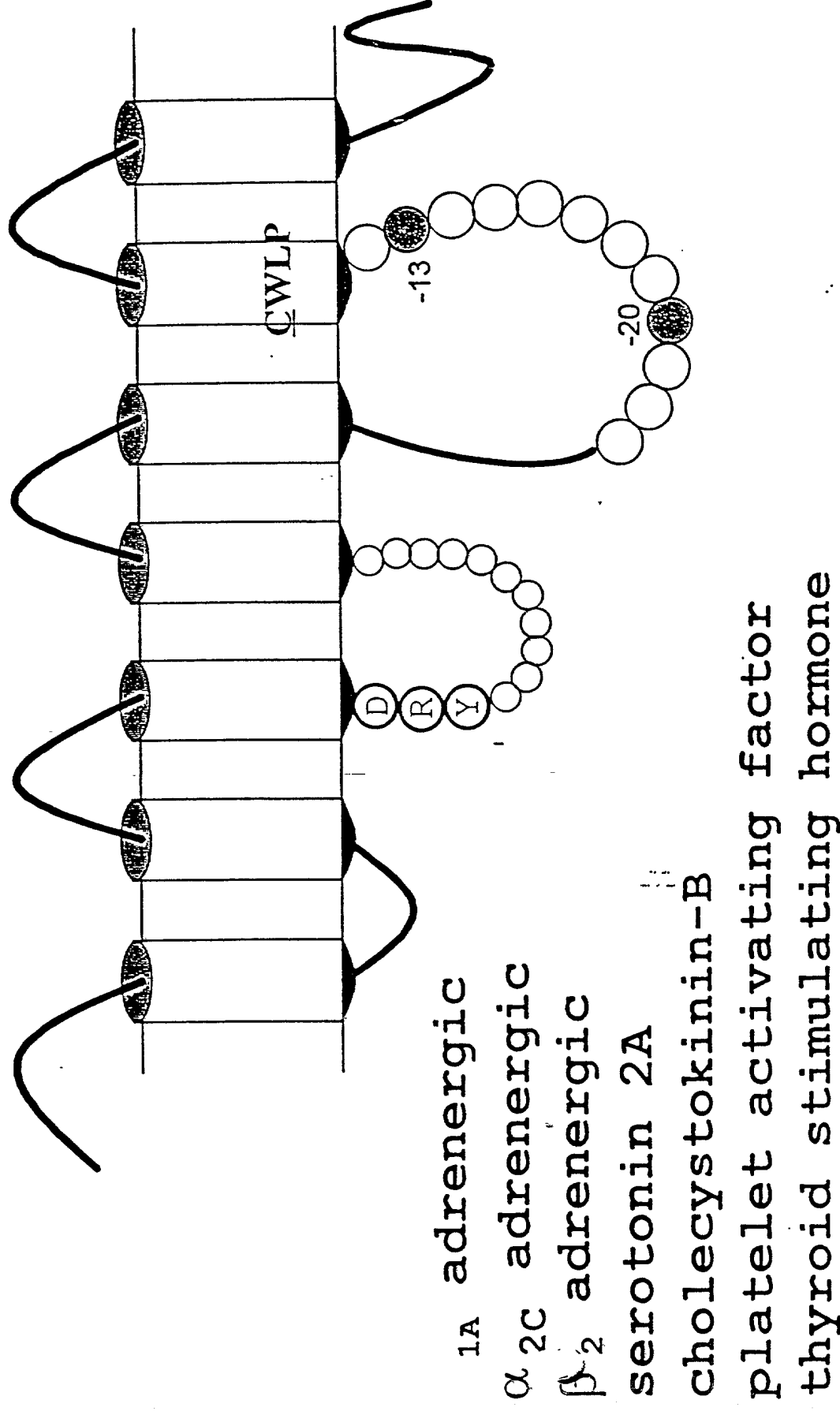


Figure 12

ork 1 -----MESPIQIFRGEPEGTCAPSACILPMSSSAWFPGWAEF..DSNGSAGSEDAQ
 orkr 1 -----MESPIQIFRGEPEGTCAPSACILPMSSSWFPMWAEF..DSNGSVGSEDDQ
 orm 1 MDSSAAPTNASNCTDAAYSSCSAPSPGSGW..MLSHLDGMLSDPCGPNRTDLGGRDSL
 ormr 1 MDSSTGPGNTSDCSDPFAQASCSPA..EGSWL..MLSHVDGMSQSDPCGLNRTGLGGRDSL
 ord 1 -----MEPAPSAGAEI..Q.PPLFNASDAYPSACPSAGANASG
 ATla 1 -----MALNSSAEDGIKRIQ
 BK-2 1 -----MFSPWKISMFLSVREDSVPTTASFSADMLNVTLOQPTLNG.TFAQ

ork 49 LEPAHISPAH..PUBITATVSKVEVWGLAGNSLWVRVIRYTKMKATNTVIFNLALADA
 orkr 49 LEPAHISPAH..PUBITATVSKVEVWGLAGNSLWVRVIRYTKMKATNTVIFNLALADA
 orm 59 CPPTGS.ESMITATITIMALYSIVCVGLFEGNPLVWVIRYTKMKATNTVIFNLALADA
 ormr 57 CPQTGS.ESMVTATITIMALYSIVCVGLFEGNPLVWVIRYTKMKATNTVIFNLALADA
 ord 37 PPGARSASSPALAHITATVSAVCAVGLAGNVLWVEGIRYTKMKATNTVIFNLALADA
 ATla 16 DDCPEAGRHSYIFVWPTIYSEIVCVGLFEGNSLWVIVLYFYMKIKTVASVELNLALADL
 BK-2 45 SKCPQVEWLGLWLNTHQPPFLWVIVVATRENIIVLSVFCLEKSSQIVAEITVGNLAADL

ork 107 LANTINPPOSATVILVN.SWPECHILCKOVISIDYAMFISIFTLTMSVDRYIACHPVK
 orkr 107 LANTINPPOSATVILVN.SWPECHILCKOVISIDYAMFISIFTLTMSVDRYIACHPVK
 orm 118 LANTINPPOSATVILVN.SWPECHILCKOVISIDYAMFISIFTLTMSVDRYIACHPVK
 ormr 116 LANTINPPOSATVILVN.SWPECHILCKOVISIDYAMFISIFTLTMSVDRYIACHPVK
 ord 97 LANTINPPOSATVILVN.SWPECHILCKOVISIDYAMFISIFTLTMSVDRYIACHPVK
 ATla 76 CFLLELWVAYTAMEYRMEGNEHCKIASASVTENYASHELIICHSEDRYIACHPVK
 BK-2 105 ILACGLARWATITISNNFDWLEGETLCAVNVNIIISMNIZSICFLMASEDRYIACHPVK

↑
 -14 from DRY *

ork 166 ALDERTPLKAKIINICIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orkr 166 ALDERTPLKAKIINICIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orm 177 ALDERTERNAKIINICIMHLLSSVCHSAIVLEGCKVR..Q..GSIDCHLTFSHPTW..HWE
 ormr 175 ALDERTERNAKIINICIMHLLSSVCHSAIVLEGCKVR..Q..GSIDCHLTFSHPTW..HWE
 ord 156 ALDERTPLKAKIINICIMHLLSSVCHSAIVLEGCKVR..D..GAVVCMIOESPSPW..WD
 ATla 136 SRLRRMLVAKVTCIILHAWAGLASIDPAVTHRV..YFIENNTITVCAHYESRN.STLP
 BK-2 165 MGRMRGVRWAKYSIVLWGCILLSSVWVFRMTKEYSDEGHNVTACVLSVPS...LIWE

ork 224 LFKKICVFEAFATVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orkr 224 LFKKICVFEAFATVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orm 232 NLFKICVFEAFATVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ormr 230 NLFKICVFEAFATVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ord 211 TVTKICVFEAFATVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ATla 193 ICGEGETKNILGSEFFPILITTSYVLSHWKALKKAYELQKNKPRND..IFRITMAIVLHFF
 BK-2 222 VFTNMLLNIVVGFALP..LSVITFCIMQIMQVLRNNEMOKFKBIQTE..RRATVILVILVILHFF

ork 284 IVCAPIPIHIFVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orkr 284 IVCAPIPIHIFVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 orm 292 IVCAPIPIHIFVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ormr 290 IVCAPIPIHIFVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ord 271 IVCAPIPIHIFVWVILITVCGIMHLLSSVCHSAIVLEGCKVR..EDVDVIECSLOEPDDDDYSWD
 ATla 250 FFSWVPHQLETFIDVILHQLGVIHDCISDIYDTAMPITICLAYFNNCANPLFYGLGKKK
 BK-2 280 IICALEFQISTFIDTLHRIGILSSCODERIIDVITQIASFVAYSNSCANPLVYVIVGKRF

ork 338 KRCEFRFCFPLKMRMEROSTSRTR.NTVOD.PAYLRDIIDGYNKPV-----
 orkr 338 KRCEFRFCFPLKMRMEROSTSRTR.NTVOD.PASMRDVGGYNKPV-----
 orm 346 KRCEFRFCFPTSSNHPQINSRHRQWV.RHESDANTVDRTNHOENLEAETAPLP
 ormr 344 KRCEFRFCFPTSSNHPQINSRHRQWV.RHESDANTVDRTNHOENLEAETAPLP
 ord 326 KRCEFRFCFPLKMRMEROSTSRTR.NTVOD.PAYLRDIIDGYNKPV-----
 ATla 310 KKYFLQLLKYUPPKAKSHS...SLSTKM..STLSYRPSDNMSSSAKKPASCFEVE-
 BK-2 340 KRKSWVYQGVCKGGCRSEPIOMENSM..GTL..RTSISVERQIHKLDWAGSRO

Figure 13

mORmouse 1 MDSSAGFCNIDSDSDPIA.PASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
mORrat 1 MDSSAGFCNIDSDSDPIA.QASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
mORbovin 1 MDSSAGFCNIDSDSDPIA.PASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
mORhuman 1 MDSSAGFCNIDSDSDPIA.PASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
mORpig 1 MDSSAGFCNIDSDSDPIA.PASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
mORws 1 MDSSAGFCNIDSDSDPIA.PASCSPA..ECSTWNLSHIDGNO SDFCGPNRTGLGGSLSLC
ATla 1 -----MALNSSAEDGKRIODDC
BK-2 1 -----MFSFWKISMFLSVREDSVPTTASFADMLNVTLOGETLNG.TFACSKC

mORmouse 58 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
mORrat 58 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
mORbovin 61 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
mORhuman 60 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
mORpig 61 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
mORws 48 PQTGSPSMVITATIALYISIVCVGLGFLVMTVIVRYTKMTATNIYIFNLALADALA
ATla 19 EKAGRHSHYIFVM.IPTLYSIFVGLGFLVMTVIVRYTKMTATNIYIFNLALADALCF
BK-2 48 PQVEWLGWNTL.IPPFLWVGLGFLVMTVIVRYTKMTATNIYIFNLALADALCF

mORmouse 118 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
mORrat 118 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
mORbovin 121 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
mORhuman 120 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
mORpig 121 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
mORws 107 TSLAPFOSVNTLMG..TWPFGLCKIVISIDYIMFTSIFTLCTMSVDRYLAVCHPVKAL
ATla 78 LLTALPLWVYTAEMEYRTPFCNHLCKIASASVTENLYASVETOLSHEDRYLAVCHPVKAL
BK-2 107 ACGLPEWNTLITISNNFDWLPGETLCAVWNTLISNNLYSSICFLMLVSDRYLAVCHPVKAL

mORmouse 177 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
mORrat 177 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
mORbovin 180 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
mORhuman 179 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
mORpig 180 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
mORws 166 DERTPRNAKIMNVCMILSSAIGLPVMTATTKYR.....GSIDCTLTFSSHPTWYWE
ATla 138 LRRITMLVAKITCTIIIMVAGLASLPVITHRNV....YFIENTNITVCAHYESRNSTLP
BK-2 167 RMRGVWAKLYSLVINGGCLLLSSPMLVFRIMK...EYSDEGHNVTAQVLSYPS..LINE

mORmouse 230 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
mORrat 230 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
mORbovin 233 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
mORhuman 232 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
mORpig 233 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
mORws 226 NALKICVFIFAFIMPVLLITVCGMLRLKSVRMLSGSKEKDRNLRRITRMVLVWVAVF
ATla 193 IGLGATKNIILGFTFPLILITSYLTKALKKAYETQKNPNDL...IFRTIMAVLLEF
BK-2 222 VFTNMLNVVGFLEP..LSVITFCTMOHVOULRNNEVQKFEIOTE..RRATVILVWVAVF

mORmouse 290 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
mORrat 290 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
mORbovin 293 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
mORhuman 292 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
mORpig 293 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
mORws 286 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF
ATla 250 FFSWVPHOITFTFDVILQGVHDCIKSDIVDTAMPITICLAYENNCLNPVLYAFIDENF
BK-2 280 IVCTPPIHIVILKALITI.....PETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENF

mORmouse 344 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
mORrat 344 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
mORbovin 347 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
mORhuman 346 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
mORpig 347 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
mORws 340 KRCSREFC...IPTSSSTIBQONSARITRONTRHPSTANTVDRTNHOLENLEAETAPLP
ATla 310 KRYLLOLLKYITPKAKSHS...SLSTKMTLSYRPSDNMSSAKKPASCFEVE----
BK-2 340 RKSWEVYQGVQKGGCRSEPIQMENSMTGL...RISIGVEROIHKLODWAGSRQ---

Figure 14

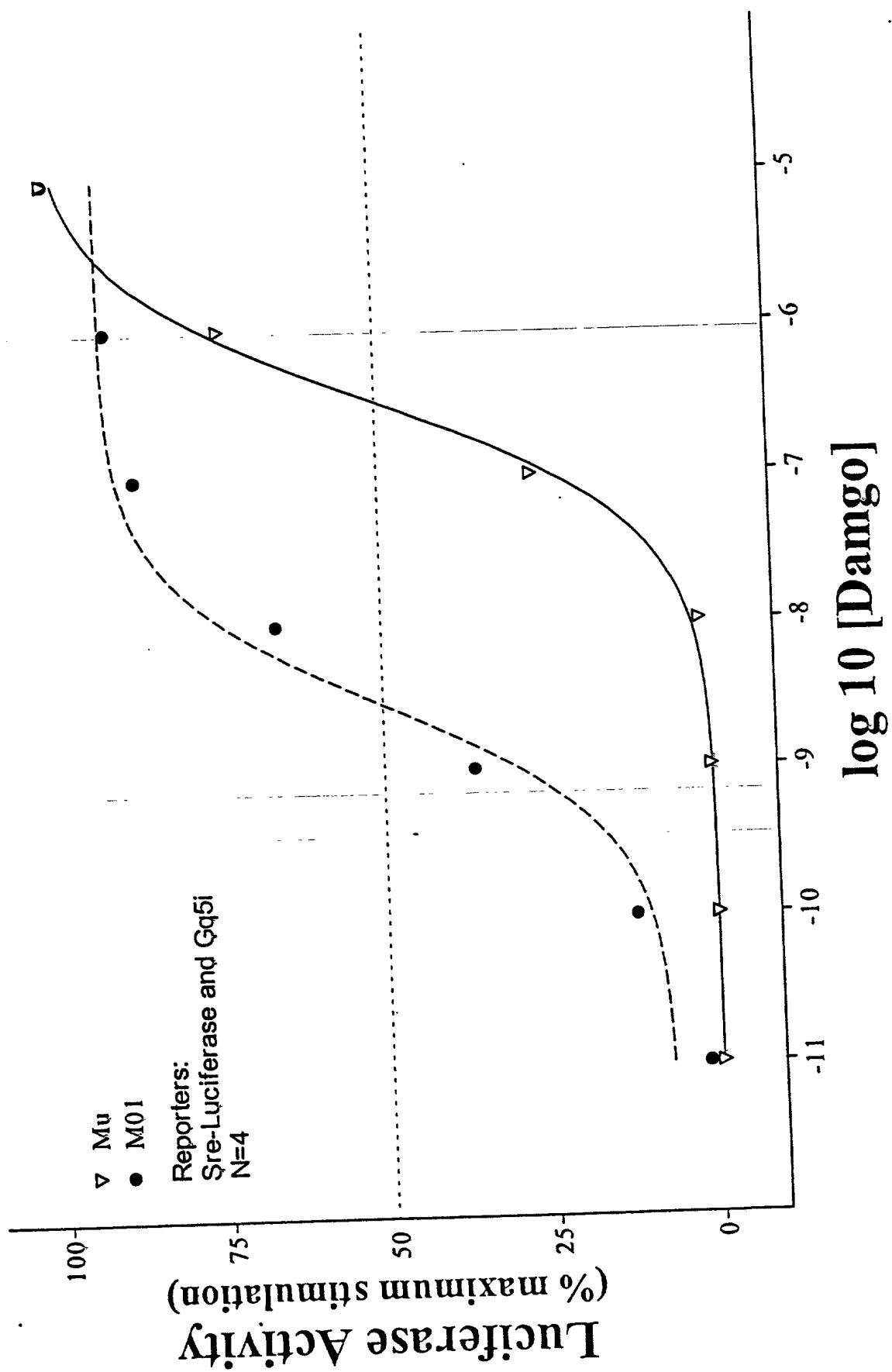


Figure 15

An Intracellular Point Mutation Results in Loss of Ligand-Induced Function

IP Production / ^3H Inositol incorporated

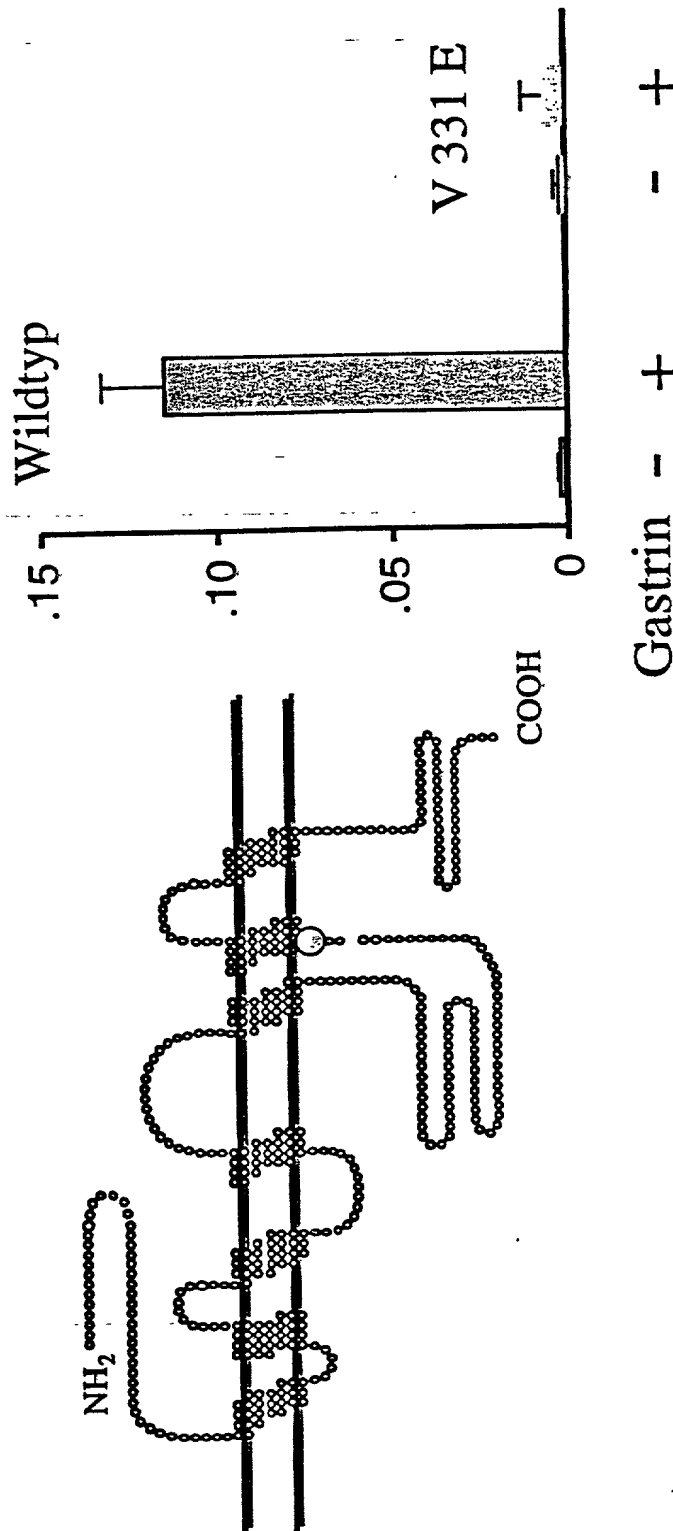


Figure 16

10039615.102507

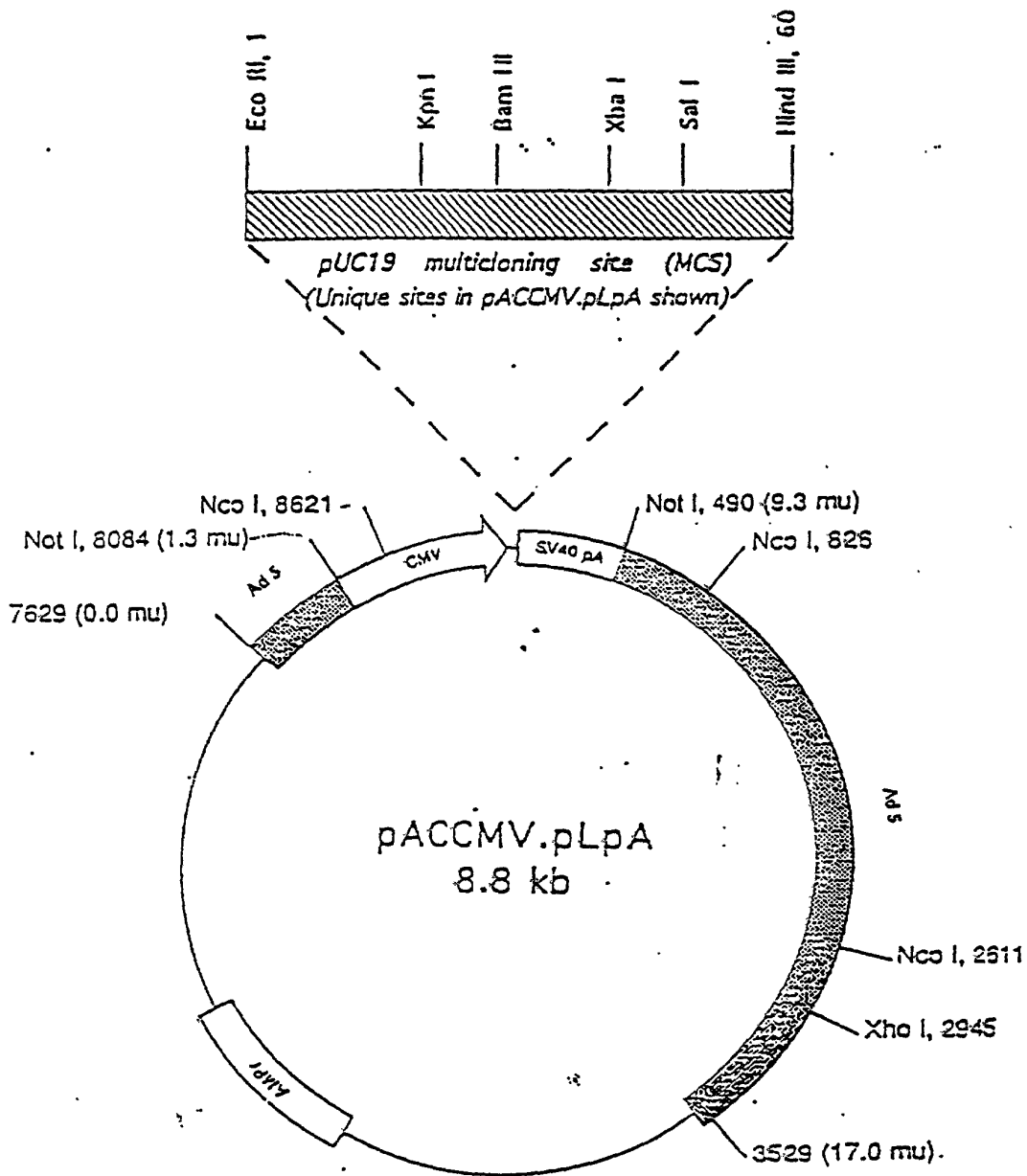


Figure 17